

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:44:03 | Search time 17.2857 Seconds  
(without alignments)  
84.405 Million cell updates/sec

Title: US-10-797-748-4

Sequence: 1 MDCCDQCTCAPDCAKADCKC 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents, PA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_CONG.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_CONG.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_CONG.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_CONG.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/6C\_CONG.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/6D\_CONG.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	22	4 US-09-948-495A-4	Sequence 4, Appl
2	147	100.0	48	4 US-09-948-495A-2	Sequence 2, Appl
3	73.5	50.0	61	4 US-09-919-039-31	Sequence 31, Appl
4	73.5	50.0	254	2 US-08-767-026-7	Sequence 7, Appl
5	73.5	50.0	254	4 US-09-319-275A-7	Sequence 7, Appl
6	70.5	48.0	61	2 US-08-785-530-5	Sequence 5, Appl
7	70.5	48.0	61	2 US-09-123-850-5	Sequence 5, Appl
8	70	47.6	61	2 US-08-785-530-4	Sequence 4, Appl
9	70	47.6	61	2 US-08-785-530-6	Sequence 6, Appl
10	70	47.6	61	2 US-09-123-850-4	Sequence 4, Appl
11	70	47.6	61	2 US-09-123-850-6	Sequence 6, Appl

12	70	47.6	62	3 US-07-780-717C-5	Sequence 5, Appl
13	69	46.9	68	1 US-07-696-051B-1	Sequence 1, Appl
14	69	46.9	68	1 US-07-924-063A-1	Sequence 1, Appl
15	69	46.9	68	1 US-08-138-340B-2	Sequence 2, Appl
16	68.5	46.6	61	4 US-09-919-039-272	Sequence 272, App
17	64.5	43.9	14	1 US-08-322-962-12	Sequence 12, Appl
18	64.5	43.9	14	3 US-08-450-653-12	Sequence 12, Appl
19	64.5	43.9	61	2 US-08-785-530-3	Sequence 3, Appl
20	64.5	43.9	61	2 US-09-123-850-3	Sequence 3, Appl
21	64.5	43.9	61	4 US-09-919-039-195	Sequence 195, App
22	64.5	43.9	1345	2 US-08-977-767-3	Sequence 3, Appl
23	64.5	43.9	2732	4 US-09-086-436-30	Sequence 30, Appl
24	63	42.9	2088	4 US-09-548-372D-13	Sequence 13, Appl
25	63	42.9	2088	4 US-09-548-367D-13	Sequence 13, Appl
26	63	42.9	2088	4 US-09-551-853D-13	Sequence 13, Appl
27	63	42.9	2088	4 US-09-548-376D-13	Sequence 13, Appl
28	63	42.9	2088	4 US-09-548-373D-13	Sequence 13, Appl
29	63	42.9	2088	4 US-09-548-366B-13	Sequence 12, Appl
30	62.5	42.5	61	4 US-09-919-039-245	Sequence 245, App
31	62	42.2	38	2 US-08-902-516-47	Sequence 47, Appl
32	62	42.2	82	4 US-09-847-185-47	Sequence 47823, A
33	61.5	41.8	82	4 US-09-270-767-32606	Sequence 32606, A
34	61.5	41.8	82	4 US-09-270-767-47823	Sequence 37, Appl
35	61.5	41.8	1400	3 US-08-630-915A-37	Sequence 37, Appl
36	61.5	41.8	1400	4 US-09-879-957-37	Sequence 7, Appl
37	61	41.5	17	1 US-08-322-962-7	Sequence 7, Appl
38	61	41.5	17	3 US-08-450-653-7	Sequence 5, Appl
39	61	41.5	75	1 US-08-322-962-5	Sequence 5, Appl
40	61	41.5	75	3 US-08-450-653-5	Sequence 5, Appl
41	61	41.5	1417	3 US-08-900-230-3	Sequence 3, Appl
42	60.5	41.2	24	1 US-08-036-555B-41	Sequence 41, Appl
43	60.5	41.2	24	1 US-08-469-569-41	Sequence 41, Appl
44	60.5	41.2	24	1 US-08-249-322A-41	Sequence 41, Appl
45	60.5	41.2	24	1 US-08-469-556A-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1  
US-09-948-495A-4  
; Sequence 4, Application US/09948495A  
; Patent No. 6750036  
; GENERAL INFORMATION:  
; APPLICANT: Acey, Roger A.  
; TITLE OF INVENTION: Metal Binding Proteins and Associated  
; FILE REFERENCE: 21089-11  
; CURRENT APPLICATION NUMBER: US/09/948,495A  
; CURRENT FILING DATE: 2001-09-06  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Fastseq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artemia  
US-09-948-495A-4

Query Match 100.0%; Score 147; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCKKDCTCAPDCKAKDKKC 22  
Db 1 MDCKKDCTCAPDCKAKDKKC 22

RESULT 2  
US-09-948-495A-2  
; Sequence 2, Application US/09948495A  
; Patent No. 6750056  
; GENERAL INFORMATION:  
; APPLICANT: Acey, Roger A.  
; TITLE OF INVENTION: Metal Binding Proteins and Associated  
; FILE OF INVENTION: Methods  
; FILE REFERENCE: 21089-11  
; CURRENT APPLICATION NUMBER: US/09/948,495A  
; CURRENT FILING DATE: 2001-09-06  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 48  
; TYPE: PAT  
; ORGANISM: Artemia  
US-09-948-495A-2

Query Match 100.0%; Score 147; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCKKDCTCAPDCKAKDKKC 22  
Db 1 MDCKKDCTCAPDCKAKDKKC 22

Search completed: December 20, 2004, 14:54:17  
Job time : 18.2857 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: December 20, 2004, 14:52:40 ; Search time 62.8571 Seconds  
(without alignments)  
125.242 Million cell updates/sec

Title: US-10-797-748-4  
Perfect score: 147  
Sequence: 1 MDCKKDCTCAPDCKAKDKKC 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 3: /cgn2\_6/ptodata/1/pubpae/US06\_NEW\_PUB.pep:\*
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  - 5: /cgn2\_6/ptodata/1/pubpae/US07\_NEW\_PUB.pep:\*
  - 6: /cgn2\_6/ptodata/1/pubpae/PCTUS\_PUBCOMB.pep:\*
  - 7: /cgn2\_6/ptodata/1/pubpae/US08\_NEW\_PUB.pep:\*
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  - 20: /cgn2\_6/ptodata/1/pubpae/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	147	100.0	22	10	US-09-948-495A-4	Sequence 4, Appl
2	147	100.0	48	10	US-09-948-495A-2	Sequence 2, Appl
3	86	58.5	64	17	US-10-425-115-26601	Sequence 264601,
4	74	50.3	2837	14	US-10-123-155-229	Sequence 229, App
5	74	50.3	2837	14	US-10-146-731-229	Sequence 229, App
6	74	50.3	2837	14	US-10-140-472-229	Sequence 229, App
7	74	50.3	2837	14	US-10-141-761-229	Sequence 229, App
8	74	50.3	2837	14	US-10-142-885-229	Sequence 229, App
9	74	50.3	2837	14	US-10-158-790-229	Sequence 229, App
10	74	50.3	2837	14	US-10-137-871-229	Sequence 229, App
11	74	50.3	2837	14	US-10-140-923-229	Sequence 229, App
12	74	50.3	2837	14	US-10-141-756-229	Sequence 229, App
13	74	50.3	2837	14	US-10-141-759-229	Sequence 229, App
14	74	50.3	2837	14	US-10-140-805-229	Sequence 229, App
15	74	50.3	2837	14	US-10-140-864-229	Sequence 229, App
16	74	50.3	2837	15	US-10-142-426-229	Sequence 229, App
17	74	50.3	3089	14	US-10-184-644-61	Sequence 61, Appl
18	74	50.3	3089	14	US-10-184-634-61	Sequence 61, Appl
19	73.5	50.0	61	10	US-09-919-039-31	Sequence 265, App
20	73.5	50.0	61	14	US-10-170-385-265	Sequence 196037,
21	73.5	50.0	61	17	US-10-425-115-196037	Sequence 1615, Ap
22	73.5	50.0	83	9	US-09-925-301-1615	Sequence 7, Appl
23	73.5	50.0	254	14	US-10-260-960-7	Sequence 217256,
24	73.5	50.0	254	14	US-10-260-562-7	Sequence 311, App
25	73	49.7	79	15	US-10-424-599-217256	Sequence 311, App
26	73	49.7	1210	14	US-10-123-155-311	Sequence 311, App
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28	73	49.7	1210	14	US-10-140-472-311	Sequence 311, App
29	73	49.7	1210	14	US-10-141-761-311	Sequence 311, App
30	73	49.7	1210	14	US-10-142-885-311	Sequence 311, App
31	73	49.7	1210	14	US-10-158-790-311	Sequence 311, App
32	73	49.7	1210	14	US-10-137-871-311	Sequence 311, App
33	73	49.7	1210	14	US-10-140-923-311	Sequence 311, App
34	73	49.7	1210	14	US-10-141-756-311	Sequence 311, App
35	73	49.7	1210	14	US-10-141-759-311	Sequence 311, App
36	73	49.7	1210	14	US-10-140-805-311	Sequence 311, App
37	73	49.7	1210	14	US-10-140-864-311	Sequence 311, App
38	73	49.7	1210	15	US-10-142-426-311	Sequence 311, App
39	73	49.7	1685	14	US-10-123-155-347	Sequence 347, App
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41	73	49.7	1685	14	US-10-140-472-347	Sequence 347, App
42	73	49.7	1685	14	US-10-141-761-347	Sequence 347, App
43	73	49.7	1685	14	US-10-142-885-347	Sequence 347, App
44	73	49.7	1685	14	US-10-158-790-347	Sequence 347, App
45	73	49.7	1685	14	US-10-137-871-347	Sequence 347, App

# ALIGNMENTS

RESULT 1  
 ; US-09-948-495A-4  
 ; Sequence 4, Application US/09948495A  
 ; Publication No. US20030105304A1

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; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948,495A
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artemia
; US-09-948-495A-4

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Query Match          100.0%; Score 147; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1,3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDCKDGGCTCAPDCKCAKDKC 22  
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DB 1 MDCKDGGCTCAPDCKCAKDKC 22

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RESULT 2
; US-09-948-495A-2
; Sequence 2, Application US/09948495A
; Publication No. US20030105304A1
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948,495A
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artemia
; US-09-948-495A-2

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Query Match          100.0%; Score 147; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 2,4e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDCKDGGCTCAPDCKCAKDKC 22  
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DB 1 MDCKDGGCTCAPDCKCAKDKC 22

Search completed: December 20, 2004, 15:09:30  
 Job time : 63.8571 secs

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:46:34 : Search time 207.743 Seconds  
(without alignments)  
117.337 Million coll updates/sec

Title: US-10-797-748-4  
Perfect score: 147  
Sequence: 1 MDCCCKDGTCAPEKCAKDCCK 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/pae/US081\_CONB.pep:++  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	22	33	US-10-797-748-4 Sequence 4, App1
2	147	100.0	48	33	US-10-797-748-2 Sequence 2, App1
3	86	58.5	60	28	US-10-219-998-59618 Sequence 59618, A
4	86	58.5	64	30	US-10-425-115-264601 Sequence 264601, A
5	81	55.1	64	22	US-09-791-537-138368 Sequence 138368, A
6	77	52.4	69	26	US-10-030-019A-258 Sequence 258, App
7	76.5	52.0	67	28	PCT-US01-04098A-3060 Sequence 3060, Ap
8	76.5	52.0	67	28	US-10-258-8992A-3060 Sequence 3060, Ap
9	76.5	52.0	67	28	US-10-293-244-3060 Sequence 3060, Ap
10	75	51.0	61	22	US-09-791-537-137656 Sequence 137656, A
11	74.5	50.7	61	22	US-09-791-537-137631 Sequence 137631, A
12	74	50.3	61	22	US-09-791-537-137731 Sequence 137731, A
13	74	50.3	67	22	US-09-791-537-138315 Sequence 138315, A
14	74	50.3	1606	36	US-60-592-191-242 Sequence 242, App
15	74	50.3	2837	27	US-10-137-871-229 Sequence 229, App
16	74	50.3	2837	27	US-10-158-790-229 Sequence 229, App
17	74	50.3	3089	27	US-10-176-912-61 Sequence 61, App1
18	74	50.3	3089	27	US-10-179-524-61 Sequence 61, App1
19	74	50.3	3089	27	US-10-184-634-61 Sequence 61, App1
20	74	50.3	3089	27	US-10-184-644-61 Sequence 61, App1
21	73.5	50.0	61	1	PCT-US01-04098A-1092 Sequence 1092, Ap
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23	73.5	50.0	61	22	US-09-791-537-137711 Sequence 137711, A
24	73.5	50.0	61	22	US-09-791-537-137780 Sequence 137780, A
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35	73.5	50.0	61	27	US-10-170-205E-29424 Sequence 29424, A
36	73.5	50.0	61	27	US-10-170-385-265 Sequence 265, App
37	73.5	50.0	61	28	US-10-258-8992A-1092 Sequence 1092, Ap
38	73.5	50.0	61	28	US-10-293-244-1092 Sequence 1092, Ap

39	73.5	50.0	61	30	US-10-425-115-196037	Sequence 196037,
40	73.5	50.0	61	31	US-10-505-928-668	Sequence 668, App
41	73.5	50.0	61	33	US-10-743-643-11	Sequence 11, Appl
42	73.5	50.0	61	36	US-60-197-873-20795	Sequence 20795, A
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ALIGNMENTS

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US-10-797-748-4
; Sequence 4, Application US/10797748
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated Methods
; FILE REFERENCE: 51302-00002
; CURRENT APPLICATION NUMBER: US/10/797,748
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 09/948,495
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PR1
; ORGANISM: Artemia sp.
US-10-797-748-4
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-797-748-2
; Sequence 2, Application US/10797748
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated Methods
; FILE REFERENCE: 51302-00002
; CURRENT APPLICATION NUMBER: US/10/797,748
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 09/948,495
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 48
; TYPE: PR1
; ORGANISM: Artemia sp.
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US-10-797-748-2

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Search completed: December 20, 2004, 15:05:24  
Job time : 208.743 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:49:24 ; Search time 10.0571 Seconds  
(without alignments)  
99.072 Million cell updates/sec

Title: US-10-797-748-4

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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 169693

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	69.5	47.3	62	6	US-10-475-075-254 Sequence 254, App
3	69.5	47.3	78	6	US-10-475-075-265 Sequence 265, App
4	69	46.9	251	6	US-10-732-923-14194 Sequence 14194, A
5	68.5	46.6	61	1	PCT-US04-36404-181 Sequence 181, App
6	68.5	46.6	61	6	US-10-972-024-161 Sequence 161, App
7	68.5	46.6	89	6	US-10-220-366A-27761 Sequence 27761, A
8	68.5	46.6	90	6	US-10-972-024-453 Sequence 453, App
9	65	44.2	35823	6	US-10-874-049-1 Sequence 1, App11

10	63	42.9	199	6	US-10-399-103A-834 Sequence 834, App
11	62.5	42.5	61	1	PCT-US04-36404-183 Sequence 183, App
12	62.5	42.5	61	1	PCT-US04-36404-186 Sequence 186, App
13	62.5	42.5	61	6	US-10-972-024-211 Sequence 211, App
14	62.5	42.5	71	6	US-10-220-366A-27416 Sequence 27416, A
15	62	42.2	35346	6	US-10-874-049-2 Sequence 2, App11
16	61.5	41.8	21	6	US-10-966-673-64 Sequence 64, App1
17	60.5	41.2	24	6	US-10-844-218-41 Sequence 41, App1
18	60.5	41.2	1076	6	US-10-955-952-219 Sequence 219, App
19	60.5	41.2	1076	6	US-10-157-779-219 Sequence 219, App
20	60.5	41.2	1076	6	US-10-964-241-219 Sequence 219, App
21	60.5	41.2	1200	1	PCT-US04-36439-18 Sequence 18, App1
22	60	40.8	1602	1	PCT-US04-33017-4 Sequence 4, App11
23	60	40.8	1602	6	US-10-962-128-4 Sequence 4, App11
24	59.5	40.5	1200	6	US-10-914-735-3 Sequence 3, App11
25	57.5	39.1	327	6	US-10-891-972-110 Sequence 110, App
26	57.5	39.1	327	6	US-10-891-972-112 Sequence 112, App
27	57.5	39.1	327	6	US-10-891-972-114 Sequence 114, App
28	57.5	39.1	327	6	US-10-891-972-116 Sequence 116, App
29	57.5	39.1	327	6	US-10-891-972-118 Sequence 118, App
30	57.5	39.1	327	6	US-10-891-972-120 Sequence 120, App
31	57.5	39.1	327	6	US-10-891-972-122 Sequence 122, App
32	57.5	39.1	327	6	US-10-891-972-124 Sequence 124, App
33	57.5	39.1	327	6	US-10-891-972-126 Sequence 126, App
34	57.5	39.1	327	6	US-10-891-972-128 Sequence 128, App
35	57.5	39.1	327	6	US-10-891-972-130 Sequence 130, App
36	57.5	39.1	327	6	US-10-891-972-132 Sequence 132, App
37	57.5	39.1	514	6	US-10-990-328-8719 Sequence 8719, Ap
38	57	38.8	28	6	US-10-915-740A-1065 Sequence 1065, Ap
39	57	38.8	111	6	US-10-220-366A-15700 Sequence 15700, A
40	56.5	38.4	1140	6	US-10-972-983-2 Sequence 2, App11
41	56.5	38.4	1140	6	US-10-408-765-1838 Sequence 1838, Ap
42	56	38.1	789	6	US-10-874-049-5 Sequence 5, App11
43	56	38.1	900	6	US-10-874-049-7 Sequence 7, App11
44	55	37.4	119	6	US-10-220-366A-1903 Sequence 1903, A
45	54.5	37.1	173	6	US-10-490-147A-6 Sequence 6, App11

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Job time : 10.0571 secs

ON protein - protein search, using sw model

Run on: December 20, 2004, 14:44:03 ; Search time 37.7143 Seconds  
(without alignments)  
84,405 Million cell updates/sec

Title: US-10-797-748-2  
Perfect score: 320  
Sequence: 1 KDCCDKCTCAPDCKAKADC.....KSPCECKEKDCSCSCGH 48

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	114.5	35.8	1400	3	US-08-630-915A-37
5	114.5	35.8	1400	4	US-09-879-957-37
6	110.5	34.5	68	1	US-07-696-051B-1
7	110.5	34.5	68	1	US-07-924-063A-1
8	110.5	34.5	68	1	US-08-138-340B-2
9	109.5	34.2	61	4	US-09-919-039-31
10	109.5	34.2	254	2	US-08-767-026-7
11	109.5	34.2	254	4	US-09-319-275A-7

12	109	34.1	2088	4	US-09-548-372D-13	Sequence 13, Appl
13	109	34.1	2088	4	US-09-548-367D-13	Sequence 19, Appl
14	109	34.1	2088	4	US-09-551-853D-13	Sequence 11, Appl
15	109	34.1	2088	4	US-09-548-376D-13	Sequence 13, Appl
16	109	34.1	2088	4	US-09-548-373D-13	Sequence 13, Appl
17	109	34.1	2088	4	US-09-548-366F-13	Sequence 13, Appl
18	107	33.4	2732	4	US-09-086-436-30	Sequence 30, Appl
19	105.5	33.0	62	3	US-07-780-717C-5	Sequence 5, Appl
20	105	32.8	1497	4	US-09-060-854B-2	Sequence 3, Appl
21	104.5	32.7	61	2	US-08-785-530-3	Sequence 3, Appl
22	104.5	32.7	61	2	US-09-123-850-3	Sequence 19, App
23	104.5	32.7	2211	3	US-09-919-039-195	Sequence 1, Appl
24	104.5	32.7	2211	4	US-10-096-961A-1	Sequence 1, Appl
25	104.5	32.7	2211	4	US-10-096-961A-1	Sequence 5, Appl
26	103.5	32.3	75	1	US-08-322-962-5	Sequence 5, Appl
27	103.5	32.3	75	3	US-08-450-653-5	Sequence 6, Appl
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32	102.5	32.0	1917	4	US-09-627-650B-5	Sequence 5, Appl
33	102.5	32.0	1917	4	US-09-436-063C-5	Sequence 5, Appl
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35	102	31.9	61	2	US-09-123-850-4	Sequence 4, Appl
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39	98.5	30.8	82	4	US-09-270-767-47823	Sequence 47823, A
40	98	30.6	120	3	US-08-508-761B-22	Sequence 22, Appl
41	96.5	30.2	908	4	US-08-714-741-44	Sequence 44, Appl
42	96.5	30.2	1345	2	US-08-977-767-3	Sequence 3, Appl
43	94.5	29.5	2508	4	US-09-627-650B-7	Sequence 7, Appl
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ALIGNMENTS

RESULT 1  
US-09-948-495A-2  
; Sequence 2, Application US/09948495A  
; Patent No. 6750056  
; GENERAL INFORMATION:  
; APPLICANT: Acey, Roger A.  
; TITLE OF INVENTION: Metal Binding Proteins and Associated  
; FILE REFERENCE: 21089-11  
; CURRENT APPLICATION NUMBER: US/09/948, 495A  
; CURRENT FILING DATE: 2001-09-06  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 48  
; TYPE: PRT  
; ORGANISM: Artemia  
US-09-948-495A-2

Query Match 100.0%; Score 320; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 9.1e-20;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Db 1 MDCKDGTCAPDCKAKDKCKGCEKSDPECKEKDCSCDCGCH 48

OM protein - protein search, using sw model  
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RESULT 2  
US-09-948-495A-4  
; Sequence 4, Application US/09948495A  
; Patent No. 6750056  
; GENERAL INFORMATION:

Title: US-10-797-748-2  
Perfect score: 320  
Sequence: 1 MDCKDGTCAPDCKAKDKC.....KSDPECKEKDCSCDCGCH 48

; APPLICANT: Acay, Roger A.  
; TITLE OF INVENTION: Metal Binding Proteins and Associated  
; FILE OF INVENTION: Methods

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

; CURRENT APPLICATION NUMBER: US/09/948,495A

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; NUMBER OF SEQ ID NOS: 10

Total number of hits satisfying chosen parameters: 1589859

; SOFTWARE: FastSeq for Windows Version 3.0

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Post-processing: Minimum Match 0%  
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and is derived by analysis of the total score distribution.





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Run on: December 20, 2004, 14:46:34 ; Search time 453.257 Seconds  
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117.337 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	136	42.5	201	18 US-09-417-507-40083	Sequence 40083, A
4	135.5	42.3	69	26 US-10-030-019A-258	Sequence 258, App
5	125	39.1	124	22 US-09-791-537-90183	Sequence 90183, A
6	125	39.1	4185	27 US-10-137-871-67	Sequence 67, Appl
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8	124	38.8	66	22 US-09-791-537-150823	Sequence 150823, A
9	121	37.8	73	22 US-09-791-537-139183	Sequence 139183, A
10	119.5	37.3	73	22 US-09-791-537-139837	Sequence 139837, A
11	119.5	37.3	73	22 US-10-137-871-429	Sequence 429, App
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13	119.5	37.3	1523	27 US-10-137-871-429	Sequence 429, App
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17	119.5	37.2	645	1 PCT-US03-26780-3122	Sequence 3122, App
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24	117.5	36.6	75	30 US-10-425-115-339798	Sequence 339798, A
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31	116.5	36.4	1536	27 US-10-176-912-461	Sequence 461, App
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33	115.5	36.1	73	22 US-09-791-537-44062	Sequence 44062, A
34	115.5	36.1	375	1 PCT-US03-26780-604	Sequence 2604, App
35	115.5	36.1	1524	27 US-10-176-912-421	Sequence 421, App
36	115.5	36.1	1524	27 US-10-176-912-421	Sequence 421, App
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38	115.5	36.1	1524	27 US-10-176-912-421	Sequence 421, App

39	115.5	36.1	2572	1	PCT-US01-12836-26	Sequence 26, Appl
40	115.5	36.1	2572	19	US-09-559-001-26	Sequence 26, Appl
41	115.5	36.1	2572	21	US-09-728-403-26	Sequence 26, Appl
42	115.5	36.1	2572	21	US-09-728-403-26	Sequence 26, Appl
43	115.5	36.1	3236	27	US-10-137-871-369	Sequence 369, App
44	115.5	36.1	3236	27	US-10-138-790-369	Sequence 369, App
45	115	35.9	2934	1	PCT-US03-26780-2987	Sequence 2987, Ap

ALIGNMENTS

RESULT 1  
US-10-797-748-2  
; Sequence 2, Application US/10797748  
; GENERAL INFORMATION:  
; APPLICANT: Acey, Roger A.  
; TITLE OF INVENTION: Metal Binding Proteins and Associated Methods  
; FILE REFERENCE: 51302-00002  
; CURRENT APPLICATION NUMBER: US/10/797,748  
; CURRENT FILING DATE: 2004-03-09  
; PRIOR APPLICATION NUMBER: 09/948,495  
; PRIOR FILING DATE: 2001-09-06  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 48  
; TYPE: PRT  
; ORGANISM: Artemia sp.  
US-10-797-748-2

Query Match 100.0%; Score 320; DB 33; Length 48;  
Best Local Similarity 100.0%; Pred. No. 3e-20;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCCKDCTCAPDCKCAKDKCKGCECKSDPECKEKCDCSCGCH 48  
Db 1 MDCCKDCTCAPDCKCAKDKCKGCECKSDPECKEKCDCSCGCH 48

RESULT 2  
US-10-797-748-4  
; Sequence 4, Application US/10797748  
; GENERAL INFORMATION:  
; APPLICANT: Acey, Roger A.  
; TITLE OF INVENTION: Metal Binding Proteins and Associated Methods  
; FILE REFERENCE: 51302-00002  
; CURRENT APPLICATION NUMBER: US/10/797,748  
; CURRENT FILING DATE: 2004-03-09  
; PRIOR APPLICATION NUMBER: 09/948,495  
; PRIOR FILING DATE: 2001-09-06  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artemia sp.

US-10-797-748-4

Query Match 45.9%; Score 147; DB 33; Length 22;  
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDCCKDCTCAPDCKCAKDKCK 22

Search completed: December 20, 2004, 15:05:23  
Job time : 455.257 secs

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OH protein - protein search, using SW model

Run on: December 20, 2004, 14:49:24 ; Search time 21.9429 Seconds  
(without alignments)  
99.072 Million cell updates/sec

Title: US-10-797-748-2

Perfect score: 320  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 169693 seqs, 45290116 residues

Total number of hits satisfying chosen parameters: 169693

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115.5	36.1	251	6	US-10-732-923-14194
2	105.5	33.0	35823	6	US-10-874-049-1
3	103	32.2	1200	1	PCT-US04-36459-18
4	102.5	32.0	62	6	US-10-475-075-254
5	101.5	31.7	61	1	PCT-US04-36404-184
6	99.5	31.1	61	1	PCT-US04-36404-181
7	99.5	31.1	61	6	US-10-972-024-161
8	99.5	31.1	89	6	US-10-220-366A-27761
9	99	30.9	900	6	US-10-874-049-7

10	98.5	30.8	61	1	PCT-US04-36404-186	Sequence 186, App
11	98.5	30.8	61	6	US-10-972-024-211	Sequence 211, App
12	98.5	30.8	71	6	US-10-220-366A-27416	Sequence 27416, A
13	98.5	30.8	90	6	US-10-972-024-453	Sequence 453, App
14	98.5	30.8	35346	6	US-10-874-049-2	Sequence 2, App11
15	97.5	30.5	1602	1	PCT-US04-33017-4	Sequence 4, App11
16	97.5	30.5	1602	6	US-10-962-128-4	Sequence 834, App
17	97	30.3	199	6	US-10-399-103A-834	Sequence 1874, Ap
18	94	29.4	62	6	US-10-408-765-1874	Sequence 183, App
19	93.5	29.2	1076	6	PCT-US04-36404-183	Sequence 219, App
20	93.5	29.2	1076	6	US-10-955-952-219	Sequence 219, App
21	93.5	29.2	1076	6	US-10-157-779-219	Sequence 219, App
22	93.5	29.2	1076	6	US-10-964-241-219	Sequence 3, App11
23	93	29.1	786	6	US-10-874-049-3	Sequence 3, App11
24	93	29.1	1200	6	US-10-914-735-3	Sequence 27094, A
25	92.5	28.9	129	6	US-10-220-366A-27094	Sequence 3, App11
26	92.5	28.9	2055	6	US-10-481-582-3	Sequence 16365, A
27	92.5	28.9	2497	6	US-10-481-582-4	Sequence 110, App
28	92	28.7	127	6	US-10-220-366A-16365	Sequence 112, App
29	91	28.4	71	6	US-10-985-299-32	Sequence 114, App
30	90	28.1	327	6	US-10-891-972-110	Sequence 116, App
31	90	28.1	327	6	US-10-891-972-112	Sequence 118, App
32	90	28.1	327	6	US-10-891-972-114	Sequence 120, App
33	90	28.1	327	6	US-10-891-972-116	Sequence 122, App
34	90	28.1	327	6	US-10-891-972-118	Sequence 124, App
35	90	28.1	327	6	US-10-891-972-120	Sequence 126, App
36	90	28.1	327	6	US-10-891-972-122	Sequence 128, App
37	90	28.1	327	6	US-10-891-972-124	Sequence 130, App
38	90	28.1	327	6	US-10-891-972-126	Sequence 132, App
39	90	28.1	327	6	US-10-891-972-128	Sequence 134, App
40	90	28.1	327	6	US-10-891-972-130	Sequence 136, App
41	90	28.1	327	6	US-10-891-972-132	Sequence 138, App
42	88.5	27.7	119	6	US-10-220-366A-14903	Sequence 140, App
43	87.5	27.3	366	6	US-10-990-328-119	Sequence 142, App
44	87.5	27.3	4040	6	US-10-990-328-10412	Sequence 144, App
45	87.5	27.3	4289	6	US-10-990-328-10414	Sequence 146, App

Search completed: December 20, 2004, 15:06:02  
Job time : 22.9429 secs